



1/39

SEQUENCE LISTING

<110> Sagami Chemical Research Center, Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661924

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

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Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly

20 25 30

Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr

35 40 45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val .

50

55

60

Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu

65

70

75

80

Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly

85

90

95

Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile

100

105

110

Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe

115

120

125

Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His

130

135

140

Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu

145

150

155

160

Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val

165

170

175

Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile

180

185

190

Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala

195

200

205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly

210

215

220

Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

225

230

235

<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1 5 10 15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp

145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu

165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu

180	185	190	
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro			
195	200	205	
Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro			
210	215	220	
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His			
225	230	235	240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr			
245	250	255	
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile			
260	265	270	
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp			
275	280	285	
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn			
290	295	300	
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys			
305	310	315	320
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr			
325	330	336	
Arg Arg Arg			

<210> 3

<211> 326

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu

1 5 10 15

Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser

20 25 30

Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro

35 40 45

Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser

50 55 60

Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

65 70 75 80

Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly

85 90 95

Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys

100 105 110

Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp

115 120 125

Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser

130 135 140

Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys

145 150 155 160

Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly

165 170 175

Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala

180 185 190

Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr

195 200 205

Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala

210 215 220
 Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
 225 230 235 240
 Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
 245 250 255
 His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
 260 265 270
 Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
 275 280 285
 Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
 290 295 300
 Phe Gin Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
 305 310 315 320
 Val Glu Glu Glu Gln Cys
 325

<210> 4

<211> 324

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu
 1 5 10 15
 Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg
 20 25 30
 Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala

35	40	45
Pro Ala Gln Gln Leu Gln	Pro Gln Pro Val Ala Val	Gln Gly Pro Glu
50	55	60
Pro Ala Arg Val Glu Lys	Ile Phe Thr Pro Ala Ala	Pro Val His Thr
65	70	75
Asn Lys Glu Asp Pro Ala	Thr Gln Thr Asn Leu Gly	Phe Ile His Ala
85	90	95
Phe Val Ala Ala Ile Ser	Val Ile Ile Val Ser Glu	Leu Gly Asp Lys
100	105	110
Thr Phe Phe Ile Ala Ala	Ile Met Ala Met Arg Tyr	Asn Arg Leu Thr
115	120	125
Val Leu Ala Gly Ala Met	Leu Ala Leu Gly Leu Met	Thr Cys Leu Ser
130	135	140
Val Leu Phe Gly Tyr Ala	Thr Thr Val Ile Pro Arg	Val Tyr Thr Tyr
145	150	155
Tyr Val Ser Thr Val Leu	Phe Ala Ile Phe Gly Ile	Arg Met Leu Arg
165	170	175
Glu Gly Leu Lys Met Ser	Pro Asp Glu Gly Gln Glu	Leu Glu Glu
180	185	190
Val Gln Ala Glu Leu Lys	Lys Lys Asp Glu Glu Phe	Gln Arg Thr Lys
195	200	205
Leu Leu Asn Gly Pro Gly	Asp Val Glu Thr Gly Thr	Ser Ile Thr Val
210	215	220
Pro Gln Lys Lys Trp Leu	His Phe Ile Ser Pro Ile	Phe Val Gln Ala
225	230	235
Leu Thr Leu Thr Phe Leu	Ala Glu Trp Gly Asp Arg	Ser Gln Leu Thr
245	250	255

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Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly

260

265

270

Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly

275

280

285

Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly

290

295

300

Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro

305

310

315

320

Asp Ser Gly Phe

<210> 5

<211> 153

<212> PRT

<213> Homo sapiens

<400> 5

Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1

5

10

15

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu

20

25

30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val

35

40

45

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu

50

55

60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gin Gly Lys Ala

65

70

75

80

Arg Leu Leu Thr His Trp Glu Gin Met Asp Tyr Gly Val Gin Phe Thr

85	90	95
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu		
100	105	110
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr		
115	120	125
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly		
130	135	140
Val Arg Ile Phe Gly Ile Asn Lys Tyr		
145	150	

<210> 6

<211> 153

<212> PRT

<213> Homo sapiens

<400> 6

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val		
1	5	10
15		
Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu		
20	25	30
Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val		
35	40	45
Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu		
50	55	60
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala		
65	70	75
80		
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr		

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85	90	95
Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu		
100	105	110
Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr		
115	120	125
Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly		
130	135	140
Val Arg Val Phe Gly Ile Asn Lys Tyr		
145	150	

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala			
1	5	10	15
Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp			
20	25	30	
Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe			
35	40	45	
Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg			
50	55	60	
Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu			
65	70	75	80
Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val			

85	90	95
Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe		
100	105	110
Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser		
115	120	125
Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val		
130	135	140
Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys		
145	150	155
Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met		160
165	170	175
Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr		
180	185	190
Leu Glu Lys Thr Ile His Glu Glu		
195	200	

<210> 8

<211> 189

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala
1 5 10 15
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
20 25 30
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu

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35 40 45
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
50 55 60
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
65 70 75 80
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
85 90 95
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
100 105 110
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
115 120 125
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
130 135 140
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
145 150 155 160
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
165 170 175
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
180 185

<210> 9

<211> 714

<212> DNA

<213> Homo sapiens

<400> 9

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 gatttggatt cctatcttaa aactcgatca ccagtcactt tcctgtctga tctgcgcagc 180
 aacctacagg tatccaatga acctgggaat cgctacaacc tccagctcat caatgcactg 240
 gtgctctatg tcgggactca ggccattgcg cacatccaca acaagggcag cacaccttca 300
 atgagcacca tcaactactc agcacacatg gatattcttc agaatttggc tgtggacttg 360
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 agccacactc actacttcag ttgcaccatg ctgtacctt ttgcagaggc caatacggaa 480
 gccatccaag aacagatcac aagagttctc ttggaacggt tgattgtaaa taggccacat 540
 ccttgggggc ttcttattac cttcattgag ctgattaaaa acccagcgtt taagttctgg 600
 aaccatgaat ttgtacactg tgccccagaa atcgaaaagt tattccagtc ggtcgcacag 660
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<210> 10

<211> 1017

<212> DNA

<213> Homo sapiens

<400> 10

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 gatgtaaaag ctcttaccct ccactatgac cgctatacca cctcccgag gctggatccc 180
 atcccacagt tgaaatgtgt tggaggcaca gctggttgtg attcttatac cccaaaagtc 240
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 ttagatattg catacaaatt tggaaaaact gtggtgagct gtgaaggcta tgagtcctct 360
 gaagaccagt atgtactaag aggttcttgt ggcttggagt ataatttaga ttatacagaa 420
 cttggcctgc agaaactgaa ggagtcctga aagcagcacg gctttgcctc tttctctgat 480
 tattattata agtggtcctc ggcggattcc tgtaacatga gtggattgat taccatcgtg 540

gtactccttg ggatcgctt tgtagtctat aagctgttcc tgagtgcagg gcagtattct 600
 cctccaccgt actctgagta tcttcattt tcccaccgtt accagagatt caccaactca 660
 gcaggacctc ctccccagg ctttaagtct gagttcacag gaccacagaa tactggccat 720
 ggtgcaactt ctggtttttg cagtgccttt acaggacaac aaggatatga aaattcagga 780
 ccagggttct ggacaggctt gggaactggt ggaatactag gatatttggt tggcagcaat 840
 agagcggcaa cacccttctc agactcgtgg tactaccctt cctatcctcc ctctaccct 900
 ggcacgtgga atagggttta ctcacccctt catggaggct cgggcagcta ttcggtatgt 960
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<210> 11

<211> 978

<212> DNA

<213> Homo sapiens

<400> 11

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 ggcacacaga aggtgcccac gccctgtgac gagaaaggct tggcagccaa gtgctttgac 180
 atgccagtgt ccctggatgg agataccaac acatccacc aggaggtggt acaatacaac 240
 tgggagactg gggatgaccg gttctccttc cggagcttcc ggagtggcat gtggctatcc 300
 tgtgaggaaa ctgtggaaga accaggggag aggtgccgaa gtttcattga acttacacca 360
 ccagccaaga gagaaatcct atggttatcc ctgggaacgc agatcaccta catcggactt 420
 caattcatca gcttcctcct gctactaaca gacttgctac tcactgggaa ccctgcctgt 480
 gggctcaaac tgagcgctt tgctgctggt tctctgtcc tgcaggtct cctggggatg 540
 gtggcccaca tgatgtattc acaagtcttc caagcgactg tcaacttggg tccagaagac 600
 tggagaccac atgtttggaa ttatggctgg gccttctaca tggcctggct ctcttcacc 660
 tgctgcatgg cgtcggctgt caccaccttc aacacgtaca ccaggatggt gctggagttc 720

aagtgc aagc atagtaagag cttcaaggaa aaccgaact gcctaccaca tcaccatcag 780
tgtttccctc ggcggtgtc aagtgcagcc cccaccgtgg gtcctttgac cagctaccac 840
cagtatcata atcagcccat ccactctgtc tctgaggag tgcacttcta ctccgagctg 900
cggaacaagg gatttcaaag aggggccagc caggagctga aagaagcagt taggtcatct 960
gtagaggaag agcagtgt 978

<210> 12

<211> 972

<212> DNA

<213> Homo sapiens

<400> 12

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caccggaaca aagaaccgcc ggcgccggcc cagcagctgc agccgcagcc tgtggctgtg 180
cagggccccg agccggcccc ggctcgagaaa atatttacac cagcagctcc agttcatacc 240
aataaagaag atcctgctac ccaaactaat ttgggattta tccatgcatt tgctgctgcc 300
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gcaatgcgct ataaccgcct gaccgtgctg gctggtgcaa tgcttgccct gggactaatg 420
acatgcttgt cagttttgtt tggctatgcc accacagtca tccccagggt ctatacatc 480
tatgtttcaa ctgtattatt tgccattttt ggcattagaa tgcttcggga aggcttaaag 540
atgagccctg atgaggggtca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600
gatgaagaat ttcaacgaac caaactttta aatggaccgg gagatgttga aacgggtaca 660
agcataacag tacctcagaa aaagtgggtg cattttatct caccattttt tgttcaagct 720
cttacattaa cattcttagc agaatggggg gatcgctctc aactaactac aattgtattg 780
gcagctagag aggaccccta tgggtgtagc gtgggtggaa ctgtggggca ctgcctgtgc 840

acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900
 acaatcatag gaggcacgtg ttttttggcg tttgcatttt ctgcactatt tataagccct 960
 gattctgggtt tt 972

<210> 13

<211> 459

<212> DNA

<213> Homo sapiens

<400> 13

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 ccgtttgtga gtgtccctgt cgtctggacc ctcaccaacc tcattcacia catgggcatg 180
 tatactctcc tgcacacggt gaaggggaca ccctttgaga ccccgaccca gggcaaggcg 240
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 ttcttgacca tcacacccat cgtgctgtac ttcctacca gcttctacac taagtacgac 360
 cagatccatt ttgtgctcaa caccgtgtcc ctgatgagcg tgcttatccc caagctgccc 420
 cagctccacg gagtccggat ttttggatc aataagtac 459

<210> 14

<211> 459

<212> DNA

<213> Homo sapiens

<400> 14

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 ggcatctggc tggcctacat catcttggtg ggattgctgc atatggttct actcagcatc 120

cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcatccataa cctggctacg 180
 tatgtcttcc ttcatacggg gaaagggaca ccctttgaga ctcttgacca aggaaaggct 240
 cggctactga cacactggga gcaaattggac tatgggctcc agtttacctc ttcccgaag 300
 ttcttcagca tctctctat tgtgctctat ctctggcca gcttctatac caagtatgat 360
 gctgcgcact tctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgccc 420
 cagttccatg gggttcgtgt ctttggcatc aacaaatac 459

<210> 15

<211> 600

<212> DNA

<213> Homo sapiens

<400> 15

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 aatatatatc aaatggcgac atttggaca acagctgggt tctctggaat attctcaaac 180
 ttctgtttca gacgctgctt caagggtaaa catgatgctt tgaagacata tgcattcattg 240
 gctacacttc catttttgtc tactgttggt actgacaagc tttttgtaat tgatgctttg 300
 tattcagata atataagcaa ggaaaactgt gttttcagaa gctcactgat tggcatagtt 360
 tgtggtgttt tctatcccag ttctttggct ttactaaaa atggacgcct ggcaaccaag 420
 tatcataccg ttccactgcc accaaaagga agggttttta tccattggat gacgctttgt 480
 caaacacaaa tgaaattaat ggcgattcct ctagtctttc agattatgtt tggaatatta 540
 aatgggtctat accattatgc agtatttgaa gagacacttg agaaaactat acatgaagag 600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

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ctcggggaca gggcgccact cacagccaca gcccacaac tggatgatga ggagatgtac 120
tcagcccaca tgcccgtca cctgcgctgt gatgcctgca gagctgtggc ttaccagatg 180
tggcaaaatc tggcaaaggc agagaccaa cttcatacct caaactctgg gggcgggcgg 240
gagctgagcg agttggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300
gactacggag ttcgagaagt ggaccaagt aaacgtctca caggcccagg acttagcgag 360
gggccagagc caagcatcag cgtgatggc acagggggcc cctggcctac caggctctcc 420
aggacatgtt tgcactactt gggggagttt ggagaagacc agatctatga agcccaccaa 480
caaggccgag gggctctgga ggcattgcta tgtgggggac cccagggggc ctgctcagag 540
aaggtgtcag ccacaagaga agagctc 567

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<210> 17

<211> 1167

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187) ... (903)

<400> 17

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ttcttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120
tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180

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ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val

1

5

10

gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276

Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe

15

20

25

30

act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324

Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu

35

40

45

aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372

Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu

50

55

60

cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420

Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn

65

70

75

gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468

Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn

80

85

90

aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516

Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met

95

100

105

110

gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat 564

Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr

115

120

125

ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac 612

Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His

130

135

140

act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat 660

Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn

145

150

155

acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg 708

Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu

160

165

170

att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag 756

Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu

175

180

185

190

ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac 804

Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His

195

200

205

tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc 852

Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys

210

215

220

atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900

Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

225

230

235

tagacgaaac tgcattctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca 960

taaactgact gaagaatcct ttcagctctt cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactggt gggatcagcc tcctgtctta tgtgggcacg ttccaaagtt 1080

taaatgcatt tttttgactc ttggccaaaa tttagaagat gctgtgaata tcattttgaa 1140

cttgtgtaaa tacatgaaag agaaaac 1167

<210> 18

<211> 1925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)... (1134)

<400> 18

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cccagggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117

Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165

Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5

10

15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213

Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20

25

30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261

Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

35

40

45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309

Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

50

55

60

65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357

Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile

70

75

80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
 230 235 240
 gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
 245 250 255
 aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
 260 265 270
 gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
 Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
 275 280 285
 tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029
 Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
 290 295 300 305
 gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
 310 315 320
 aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
 325 330 335
 aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatattt 1180
 Arg Arg

 tcatacacttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt 1240
 caaaagtctt gtggtgttat gtccagtgtg gctttttgta ttctattatt tgaggctaaa 1300
 agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt 1360
 gcagtttttg aaagtgatca ttactgtgga atgctaataaa tacattaatt tctaaaacct 1420

gtgatgccct aagaagcatt aagaatgaag gtgttgact aatagaaact aagtacagaa 1480
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 ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca 1660
 gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata 1720
 agcatctaga aggttggtgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1780
 tttctttcgt tcataagagg taaaggtcaa atttttcaac aaaagtcttt taataacaaa 1840
 agcatgcagt tctctgtgaa atctcaaata ttgttgaat agtctgtttc aatcttaaaa 1900
 agaatcaata aaaacaaaca agggg 1925

<210> 19

<211> 1125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (71)...(1051)

<400> 19

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gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln

1

5

10

cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157

Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser

15

20

25

25/39

aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205

Thr	Thr	Ser	Leu	Leu	Ser	Asn	Tyr	Trp	Phe	Val	Gly	Thr	Gln	Lys	Val	
30					35					40					45	
ccc	aag	ccc	ctg	tgc	gag	aaa	ggt	ctg	gca	gcc	aag	tgc	ttt	gac	atg	253
Pro	Lys	Pro	Leu	Cys	Glu	Lys	Gly	Leu	Ala	Ala	Lys	Cys	Phe	Asp	Met	
				50					55					60		
cca	gtg	tcc	ctg	gat	gga	gat	acc	aac	aca	tcc	acc	cag	gag	gtg	gta	301
Pro	Val	Ser	Leu	Asp	Gly	Asp	Thr	Asn	Thr	Ser	Thr	Gln	Glu	Val	Val	
				65					70					75		
caa	tac	aac	tgg	gag	act	ggg	gat	gac	cgg	ttc	tcc	ttc	cgg	agc	ttc	349
Gln	Tyr	Asn	Trp	Glu	Thr	Gly	Asp	Asp	Arg	Phe	Ser	Phe	Arg	Ser	Phe	
		80						85						90		
cgg	agt	ggc	atg	tgg	cta	tcc	tgt	gag	gaa	act	gtg	gaa	gaa	cca	ggg	397
Arg	Ser	Gly	Met	Trp	Leu	Ser	Cys	Glu	Glu	Thr	Val	Glu	Glu	Pro	Gly	
		95					100							105		
gag	agg	tgc	cga	agt	ttc	att	gaa	ctt	aca	cca	cca	gcc	aag	aga	gaa	445
Glu	Arg	Cys	Arg	Ser	Phe	Ile	Glu	Leu	Thr	Pro	Pro	Ala	Lys	Arg	Glu	
110					115					120				125		
atc	cta	tgg	tta	tcc	ctg	gga	acg	cag	atc	acc	tac	atc	gga	ctt	caa	493
Ile	Leu	Trp	Leu	Ser	Leu	Gly	Thr	Gln	Ile	Thr	Tyr	Ile	Gly	Leu	Gln	
				130					135					140		
ttc	atc	agc	ttc	ctc	ctg	cta	cta	aca	gac	ttg	cta	ctc	act	ggg	aac	541
Phe	Ile	Ser	Phe	Leu	Leu	Leu	Leu	Thr	Asp	Leu	Leu	Leu	Thr	Gly	Asn	
				145					150					155		
cct	gcc	tgt	ggg	ctc	aaa	ctg	agc	gcc	ttt	gct	gct	gtt	tcc	tct	gtc	589
Pro	Ala	Cys	Gly	Leu	Lys	Leu	Ser	Ala	Phe	Ala	Ala	Val	Ser	Ser	Val	
				160					165					170		
ctg	tca	ggt	ctc	ctg	ggg	atg	gtg	gcc	cac	atg	atg	tat	tca	caa	gtc	637

Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
 175 180 185
 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
 190 195 200 205
 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
 210 215 220
 tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
 225 230 235
 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
 240 245 250
 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
 255 260 265
 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
 270 275 280 285
 ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973
 Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg
 290 295 300
 aac aag gga tit caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt 1021
 Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val
 305 310 315
 agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg 1070

Arg Ser Ser Val Glu Glu Glu Gln Cys

320

325

agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc 1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)...(1014)

<400> 20

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Met Ala Ala Ala Ala

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ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102

Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu

10

15

20

gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa 150

Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu

25

30

35

gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg 198

Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu

40

45

50

cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag 246

Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu
 55 60 65
 aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cet 294
 Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro
 70 75 80 85
 gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata 342
 Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile
 90 95 100
 tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca 390
 Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala
 105 110 115
 gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca 438
 Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala
 120 125 130
 atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat 486
 Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr
 135 140 145
 gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta 534
 Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val
 150 155 160 165
 tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg 582
 Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
 170 175 180
 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta 630
 Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
 185 190 195
 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg 678

Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
 200 205 210
 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg 726
 Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
 215 220 225
 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc 774
 Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
 230 235 240 245
 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca 822
 Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
 250 255 260
 gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac 870
 Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
 265 270 275
 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag 918
 Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
 280 285 290
 aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg 966
 Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu
 295 300 305
 gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt 1011
 Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe
 310 315 320
 taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat 1070
 agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtagcac tgattttgtg 1130
 agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt 1190
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 tcaatatttg acaatgtgga attaccaaatt taaaagagaa tactatgaat gtattcatat 1670
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 cagt 1734

<210> 21

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)...(559)

<400> 21

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 cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca 112

Met Asn Val Gly Thr

1

5

gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc . 160

Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly

atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg 208
 Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu
 25 30 35
 ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac 256
 Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn
 40 45 50
 ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg 304
 Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly
 55 60 65
 aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac 352
 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
 70 75 80 85
 tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc 400
 Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe
 90 95 100
 ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act 448
 Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr
 105 110 115
 aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc 496
 Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser
 120 125 130
 gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga 544
 Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly
 135 140 145
 atc aat aag tac tgagagtgca gcccttccc ctgccaggg tggcagggga gggg 600
 Ile Asn Lys Tyr

tagggtaaaa ggcattgtgct gcaacactga agacagaaag aagaagcctc tggacactgc 660
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 tgggtccctg tgcctcttc caggggtcca agggaacagg agaggtcact gggcctgttt 1920
 tctccctcct gaccctgcat ctccacccc gtgtatcata gggaaacttt accttaaaat 1980
 ctttctaagc aaagtgtgaa taggattttt actcccttg tacagtattc tgagaaacgc 2040
 aaataaaagg gcaacatggt tctg 2064

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)...(489)

<400> 22

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Met Asn Val Gly Val Ala His Ser

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5

gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg 99

Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu

10

15

20

gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc 147

Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile

25

30

35

40

ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat 195

Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His

45

50

55

aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt 243

Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe

60

65

70

gag act cct gac caa gga aag gct cgg cta ctg aca cac tgg gag caa 291

Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln

75

80

85

atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc 339
 Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile
 90 95 100
 tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat 387
 Ser Pro Ile Val Leu Tyr Leu Leu Ala Ser Phe Tyr Thr Lys Tyr Asp
 105 110 115 120
 gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg 435
 Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu
 125 130 135
 ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa 483
 Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys
 140 145 150
 tac tgag ggatggggttt tgggacagct ccatgggcat ggggaaggca ctgaaacaga 540
 Tyr

ggactataaaa acatccttct cttattctcc 570

<210> 23

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (278)... (880)

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Met Ala Ala Ser Met

1

5

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His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro

10

15

20

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Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu

25

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Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly

40

45

50

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Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val

55

60

65

aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt 532

Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe

70

75

80

85

ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat 580

Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr

90

95

100

tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att 628

Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile

105	110	115	
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Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys			
120	125	130	
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa			724
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys			
135	140	145	
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Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys			
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tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat			820
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn			
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Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile			
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His Glu Glu			
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Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
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Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
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Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
      50              55              60
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg      297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
      65              70              75              80
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc      345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Ara Ser Cys Ser
      85              90              95

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 ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125
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 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140
 cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa 537
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
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 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
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